```
=> fil reg; d que l2

FILE 'REGISTRY' ENTERED AT 14:59:43 ON 11 MAY 2000
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STRUCTURE FILE UPDATES:   10 MAY 2000  HIGHEST RN 264236-91-1
DICTIONARY FILE UPDATES:  10 MAY 2000  HIGHEST RN 264236-91-1

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 11, 2000

  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.

Structure search limits have been increased.  See HELP SLIMIT
for details.

L2            75 SEA FILE=REGISTRY ABB=ON  [YF]..C...C.{10-12}C...C...[YF]C..C.
                 ..C.{10-12}C...C...C/SQSP


=> d cn rn sql l2 1-75; fil capl; d que l3

L2   ANSWER 1 OF 75  REGISTRY  COPYRIGHT 2000 ACS
CN   INDEX NAME NOT YET ASSIGNED
RN   263557-82-0  REGISTRY
SQL  47

L2   ANSWER 2 OF 75  REGISTRY  COPYRIGHT 2000 ACS
CN   INDEX NAME NOT YET ASSIGNED
RN   263557-66-0  REGISTRY
SQL  43

L2   ANSWER 3 OF 75  REGISTRY  COPYRIGHT 2000 ACS
CN   INDEX NAME NOT YET ASSIGNED
RN   263557-65-9  REGISTRY
SQL  43

L2   ANSWER 4 OF 75  REGISTRY  COPYRIGHT 2000 ACS
CN   INDEX NAME NOT YET ASSIGNED
RN   263489-51-6  REGISTRY
SQL  72

L2   ANSWER 5 OF 75  REGISTRY  COPYRIGHT 2000 ACS
CN   INDEX NAME NOT YET ASSIGNED
RN   263489-50-5  REGISTRY
SQL  74

L2   ANSWER 6 OF 75  REGISTRY  COPYRIGHT 2000 ACS
CN   INDEX NAME NOT YET ASSIGNED
RN   263132-70-3  REGISTRY
SQL  580

L2   ANSWER 7 OF 75  REGISTRY  COPYRIGHT 2000 ACS
CN   INDEX NAME NOT YET ASSIGNED
RN   263104-93-4  REGISTRY
SQL  821

L2   ANSWER 8 OF 75  REGISTRY  COPYRIGHT 2000 ACS
```

claim 17 or claim 18 (cols 37-39) claim 1

Hope -
It costs ~ $5 to display each sequence in Registry. The cost would have been unreasonable ~~for this answer~~ to display 75 answers.
Look through the citations from CAPLUS. If there are any that look good, bring the search back to me & I will display the seqs for that (those) references. This can be done quickly, while you wait.
Barb

CN Protein MiAMP2c (Macadamia integrifolia clone 3 gene AMP2 isoform 3) (9CI) (CA INDEX NAME)
RN 262434-56-0 REGISTRY
SQL 67

L2 ANSWER 9 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN INDEX NAME NOT YET ASSIGNED
OTHER NAMES:
CN Peptide MiAMP2c (Macadamia integrifolia clone 3 gene AMP2 isoform 2)
RN 262433-71-6 REGISTRY
SQL 47

L2 ANSWER 10 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN INDEX NAME NOT YET ASSIGNED
OTHER NAMES:
CN Peptide MiAMP2c (Macadamia integrifolia clone 3 gene AMP2 isoform 1)
RN 262433-70-5 REGISTRY
SQL 45

L2 ANSWER 11 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN INDEX NAME NOT YET ASSIGNED
OTHER NAMES:
CN Peptide MiAMP2b (Macadamia integrifolia clone 1 gene AMP2)
RN 262433-66-9 REGISTRY
SQL 41

L2 ANSWER 12 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (Porphyromonas gingivalis strain ATCC 33277 protein (histidine) kinase gene plus flanks) (9CI) (CA INDEX NAME)
RN 260773-72-6 REGISTRY
SQL 2300

L2 ANSWER 13 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (human clone DNA59219-1613 protein PRO1359 cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 106: PN: WO0012708 FIGURE: 33 claimed protein
CN DNA (human clone DNA59219-1613 protein UNQ708 cDNA plus flanks)
RN 260533-83-3 REGISTRY
SQL 2401

L2 ANSWER 14 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN 42: PN: WO0011187 FIGURE: 4B unclaimed protein (9CI) (CA INDEX NAME)
RN 260383-95-7 REGISTRY
SQL 298

L2 ANSWER 15 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN 40: PN: WO0011187 FIGURE: 4A unclaimed protein (9CI) (CA INDEX NAME)
RN 260383-93-5 REGISTRY
SQL 444

L2 ANSWER 16 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN 77: PN: US6018030 SEQID: 91 unclaimed protein (9CI) (CA INDEX NAME)
RN 255900-75-5 REGISTRY
SQL 47

L2 ANSWER 17 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (synthetic Aequorea victoria green fluorescent protein) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: US6020192 SEQID: 3 claimed protein
RN 255704-94-0 REGISTRY

SQL 717

L2 ANSWER 18 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (Drosophila melanogaster presenilin cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 12: PN: US5986054 SEQID: 165 claimed protein
RN 250242-56-9 REGISTRY
SQL 1895

L2 ANSWER 19 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Protein (human bladder fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9954460 SEQID: 357 claimed protein
RN 249906-26-1 REGISTRY
SQL 169

L2 ANSWER 20 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (Solanum tuberosum clone Ac64 gene Rx protein cDNA) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9954490 FIGURE: 7A claimed sequence
RN 249577-46-6 REGISTRY
SQL 3201

L2 ANSWER 21 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (Solanum tuberosum clone Ac64 gene Rx protein cDNA) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9954490 FIGURE: 7A claimed sequence
RN 249577-44-4 REGISTRY
SQL 3229

L2 ANSWER 22 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (Solanum tuberosum clone Acl5 gene Rx protein cDNA) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9954490 FIGURE: 7A claimed sequence
RN 249577-41-1 REGISTRY
SQL 3230

L2 ANSWER 23 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (Solanum tuberosum clone 221h2 gene Rx protein cDNA) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9954490 FIGURE: 7A claimed sequence
RN 249577-38-6 REGISTRY
SQL 3214

L2 ANSWER 24 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (Solanum tuberosum clone 111h1 gene Rx protein cDNA) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9954490 FIGURE: 7A claimed sequence
RN 249577-36-4 REGISTRY
SQL 3254

L2 ANSWER 25 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN PN: WO9954490 FIGURE: 7A unclaimed sequence (9CI) (CA INDEX NAME)
RN 249569-21-9 REGISTRY
SQL 3220

L2 ANSWER 26 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN PN: WO9954490 FIG: 7A unclaimed protein (9CI) (CA INDEX NAME)
RN 249569-19-5 REGISTRY
SQL 3231

L2 ANSWER 27 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN PN: US5972684 SEQID: 3 unclaimed protein (9CI) (CA INDEX NAME)
RN 249299-76-1 REGISTRY
SQL 1345

L2 ANSWER 28 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Secretory protein (human clone 153 precursor N-terminal fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9953051 SEQID: 941 claimed protein
RN 247017-76-1 REGISTRY
SQL 66

L2 ANSWER 29 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (Mycobacterium tuberculosis antigen Ra12 fusion protein with Mycobacterium tuberculosis antigen TbH9 fusion protein with Mycobacterium tuberculosis antigen Ra35-specifying) (9CI) (CA INDEX NAME)
RN 246852-79-9 REGISTRY
SQL 2166

L2 ANSWER 30 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN PN: WO9951728 SEQID: 4 unclaimed protein (9CI) (CA INDEX NAME)
RN 246036-79-3 REGISTRY
SQL 415

L2 ANSWER 31 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (human erythropoietin cDNA 5'-flank 224-nucleotide fragment) (9CI) (CA INDEX NAME)
RN 234439-19-1 REGISTRY
SQL 215

L2 ANSWER 32 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (human gene CtIP protein CtIP (CtBP-interacting protein)) (9CI) (CA INDEX NAME)
RN 227188-49-0 REGISTRY
SQL 2694

L2 ANSWER 33 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (human 397-465-conductin-specifying cDNA) (9CI) (CA INDEX NAME)
RN 221220-54-8 REGISTRY
SQL 207

L2 ANSWER 34 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (human nuclear receptor nNR2 cDNA) (9CI) (CA INDEX NAME)
RN 221111-80-4 REGISTRY
SQL 1257

L2 ANSWER 35 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (human clone HM74a G protein-coupled receptor cDNA plus flanks) (9CI) (CA INDEX NAME)
RN 217945-23-8 REGISTRY
SQL 1360

L2 ANSWER 36 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (human KG-1 cell gene ha1217 protein cDNA) (9CI) (CA INDEX NAME)
RN 215728-51-1 REGISTRY
SQL 2946

L2 ANSWER 37 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN 117-185-Antimicrobial protein MiAMP2c (Macadamia integrifolia clone 1 precursor) (9CI) (CA INDEX NAME)
RN 209909-73-9 REGISTRY
SQL 69

L2 ANSWER 38 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN 76-144-Antimicrobial protein MiAMP2c (Macadamia integrifolia clone 3 precursor C-terminal fragment) (9CI) (CA INDEX NAME)
RN 209909-72-8 REGISTRY
SQL 69

L2 ANSWER 39 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN 117-185-Antimicrobial protein MiAMP2c (Macadamia integrifolia clone 2 precursor) (9CI) (CA INDEX NAME)
RN 209909-71-7 REGISTRY
SQL 69

L2 ANSWER 40 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN 81-140-Antimicrobial protein TcAMP1 (Theobroma cacao fragment) (9CI) (CA INDEX NAME)
RN 209909-68-2 REGISTRY
SQL 60

L2 ANSWER 41 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN L-Glutamic acid, L-tyrosyl-L-.alpha.-glutamyl-L-arginyl-L-.alpha.-aspartyl-L-prolyl-L-arginyl-L-glutaminyl-L-glutaminyl-L-tyrosyl-L-.alpha.-glutamyl-L-glutaminyl-L-cysteinyl-L-glutaminyl-L-arginyl-L-arginyl-L-cysteinyl-L-.alpha.-glutamyl-L-seryl-L-.alpha.-glutamyl-L-alanyl-L-threonyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-arginyl-L-.alpha.-glutamyl-L-glutaminyl-L-.alpha.-glutamyl-L-glutaminyl-L-cysteinyl-L-.alpha.-glutamyl-L-glutaminyl-L-arginyl-L-cysteinyl-L-.alpha.-glutamyl-L-arginyl-L-.alpha.-glutamyl-L-tyrosyl-L-lysyl-L-.alpha.-glutamyl-L-glutaminyl-L-glutaminyl-L-arginyl-L-glutaminyl-L-glutaminyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 34-80-Antimicrobial protein TcAMP1 (Theobroma cacao fragment)
RN 209909-60-4 REGISTRY
SQL 47

L2 ANSWER 42 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN L-Aspartic acid, L-seryl-L-.alpha.-glutamyl-L-phenylalanyl-L-.alpha.-aspartyl-L-arginyl-L-glutaminyl-L-.alpha.-glutamyl-L-tyrosyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-cysteinyl-L-lysyl-L-arginyl-L-glutaminyl-L-cysteinyl-L-methionyl-L-glutaminyl-L-leucyl-L-.alpha.-glutamyl-L-threonyl-L-serylglycyl-L-glutaminyl-L-methionyl-L-arginyl-L-arginyl-L-cysteinyl-L-valyl-L-seryl-L-glutaminyl-L-cysteinyl-L-.alpha.-aspartyl-L-lysyl-L-arginyl-L-phenylalanyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-isoleucyl-L-.alpha.-aspartyl-L-tryptophyl-L-seryl-L-lysyl-L-tyrosyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 29-73-Antimicrobial protein MiAMP2c (Macadamia integrifolia clone 1 precursor)
RN 209909-59-1 REGISTRY
SQL 45

L2 ANSWER 43 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN L-Arginine, L-seryl-L-glutaminyl-L-arginyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-.alpha.-glutamyl-L-cysteinyl-L-glutaminyl-L-glutaminyl-L-histidyl-L-cysteinyl-L-histidyl-L-glutaminyl-L-glutaminyl-L-.alpha.-glutamyl-L-glutaminyl-L-arginyl-L-prolyl-L-.alpha.-glutamyl-L-lysyl-L-

lysyl-L-glutaminyl-L-glutaminyl-L-cysteinyl-L-valyl-L-arginyl-L-.alpha.-glutamyl-L-cysteinyl-L-arginyl-L-.alpha.-glutamyl-L-lysyl-L-tyrosyl-L-glutaminyl-L-.alpha.-glutamyl-L-asparaginyl-L-prolyl-L-tryptophyl-L-arginylglycyl-L-.alpha.-glutamyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 120-161-Antimicrobial protein GhAMP1 (cotton)
RN 209909-58-0 REGISTRY
SQL 42

L2 ANSWER 44 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN L-Tyrosine, L-asparaginyl-L-glutaminyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-prolyl-L-glutaminyl-L-threonyl-L-.alpha.-glutamyl-L-cysteinyl-L-glutaminyl-L-glutaminyl-L-cysteinyl-L-glutaminyl-L-arginyl-L-arginyl-L-cysteinyl-L-arginyl-L-glutaminyl-L-glutaminyl-L-.alpha.-glutamyl-L-seryl-L-.alpha.-aspartyl-L-prolyl-L-arginyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-tyrosyl-L-cysteinyl-L-glutaminyl-L-arginyl-L-arginyl-L-cysteinyl-L-lysyl-L-.alpha.-glutamyl-L-isoleucyl-L-cysteinyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 33-75-Antimicrobial protein MiAMP2c (Macadamia integrifolia clone 3 precursor C-terminal fragment)
RN 209909-57-9 REGISTRY
SQL 43

L2 ANSWER 45 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN L-Tyrosine, L-asparaginyl-L-glutaminyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-prolyl-L-glutaminyl-L-threonyl-L-.alpha.-glutamyl-L-cysteinyl-L-glutaminyl-L-glutaminyl-L-cysteinyl-L-glutaminyl-L-arginyl-L-arginyl-L-cysteinyl-L-arginyl-L-glutaminyl-L-glutaminyl-L-.alpha.-glutamyl-L-serylglycyl-L-prolyl-L-arginyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-tyrosyl-L-cysteinyl-L-glutaminyl-L-arginyl-L-arginyl-L-cysteinyl-L-lysyl-L-.alpha.-glutamyl-L-isoleucyl-L-cysteinyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 74-116-Antimicrobial protein MiAMP2c (Macadamia integrifolia clone 1 precursor)
RN 209909-56-8 REGISTRY
SQL 43

L2 ANSWER 46 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN L-Tyrosine, L-asparaginyl-L-glutaminyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-prolyl-L-glutaminyl-L-threonyl-L-.alpha.-aspartyl-L-cysteinyl-L-glutaminyl-L-glutaminyl-L-cysteinyl-L-glutaminyl-L-arginyl-L-arginyl-L-cysteinyl-L-arginyl-L-glutaminyl-L-glutaminyl-L-.alpha.-glutamyl-L-serylglycyl-L-prolyl-L-arginyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-tyrosyl-L-cysteinyl-L-glutaminyl-L-arginyl-L-arginyl-L-cysteinyl-L-lysyl-L-.alpha.-glutamyl-L-isoleucyl-L-cysteinyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 74-116-Antimicrobial protein MiAMP2c (Macadamia integrifolia clone 2 precursor)
RN 209909-55-7 REGISTRY
SQL 43

L2 ANSWER 47 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN L-Glutamine, L-prolyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-prolyl-L-glutaminyl-L-arginyl-L-arginyl-L-tyrosyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-cysteinyl-L-glutaminyl-L-glutaminyl-L-.alpha.-glutamyl-L-cysteinyl-L-arginyl-L-glutaminyl-L-glutaminyl-L-.alpha.-glutamyl-L-.alpha.-

glutamyl-L-arginyl-L-glutaminyl-L-glutaminyl-L-prolyl-L-glutaminyl-L-cysteinyl-L-glutaminyl-L-glutaminyl-L-arginyl-L-cysteinyl-L-leucyl-L-lysyl-L-arginyl-L-phenylalanyl-L-.alpha.-glutamyl-L-glutaminyl-L-.alpha.-glutamyl-L-glutaminyl-L-glutaminyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 33-79-Antimicrobial protein GhAMP1 (cotton)
RN 209909-54-6 REGISTRY
SQL 40

L2 ANSWER 48 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Antimicrobial protein GhAMP1 (cotton) (9CI) (CA INDEX NAME)
RN 209902-59-0 REGISTRY
SQL 590

L2 ANSWER 49 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Antimicrobial protein TcAMP1 (Theobroma cacao fragment) (9CI) (CA INDEX NAME)
RN 209902-58-9 REGISTRY
SQL 525

L2 ANSWER 50 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Antimicrobial protein MiAMP2c (Macadamia integrifolia clone 3 precursor C-terminal fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF161885-derived protein GI 5852876
CN MiAMP2 antimicrobial peptide (Macadamia integrifolia clone 2 gene AMP2 precursor C-terminal fragment)
CN Vicilin MiAMP2 (Macadamia integrifolia clone 3 gene AMP2 precurso C-terminal fragment)
RN 209902-56-7 REGISTRY
SQL 625

L2 ANSWER 51 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Antimicrobial protein MiAMP2c (Macadamia integrifolia clone 2 precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF161884-derived protein GI 5852874
CN MiAMP2 antimicrobial peptide (Macadamia integrifolia clone 2 gene AMP2 precursor)
CN Vicilin MiAMP2 (Macadamia integrifolia clone 2 gene AMP2 precursor)
RN 209902-52-3 REGISTRY
SQL 666

L2 ANSWER 52 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Antimicrobial protein MiAMP2c (Macadamia integrifolia clone 1 precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF161883-derived protein GI 5852872
CN MiAMP2 antimicrobial peptide (Macadamia integrifolia clone 1 gene AMP2 precursor)
CN Vicilin MiAMP2 (Macadamia integrifolia clone 1 gene AMP2 precursor)
RN 209902-50-1 REGISTRY
SQL 666

L2 ANSWER 53 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Protein (Treponema pallidum gene TP0856) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AE001256-derived protein GI 3323176
RN 209611-36-9 REGISTRY
SQL 325

L2 ANSWER 54 OF 75 REGISTRY COPYRIGHT 2000 ACS

CN DNA (gram-negative bacteria strain E-396 .beta.-carotene oxygenase gene crtZE396) (9CI) (CA INDEX NAME)
RN 209540-18-1 REGISTRY
SQL 486

L2 ANSWER 55 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (gram-negative bacteria strain E-396 .beta.-carotene .beta.4-oxygenase gene crtWE396) (9CI) (CA INDEX NAME)
RN 209540-17-0 REGISTRY
SQL 729

L2 ANSWER 56 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Protein (Caenorhabditis elegans clone ZK1251 gene ZK1251.2) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank Z68222-derived protein GI 1122848
CN Insulin-like protein ZK1251.2, prepro- (Caenorhabditis elegans)
CN PN: WO9954436 SEQID: 8 claimed protein
CN Preproinsulin homolog (Caenorhabditis elegans clone ZK1251 gene ZK1251.2 reduced)
RN 207465-94-9 REGISTRY
SQL 105

L2 ANSWER 57 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (mouse strain B10.S H-2Dq gene 5'-regulatory region) (9CI) (CA INDEX NAME)
RN 197981-22-9 REGISTRY
SQL 84

L2 ANSWER 58 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (Oryza sativa japonica strain Zhonghua-8 Bowman-Birk proteinase inhibitor gene RBBI plus flanks) (9CI) (CA INDEX NAME)
RN 188900-56-3 REGISTRY
SQL 415

L2 ANSWER 59 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN DNA (Dolichovespula maculata hyaluronidase C-terminal fragment-specifying cDNA) (9CI) (CA INDEX NAME)
RN 186986-50-5 REGISTRY
SQL 993

L2 ANSWER 60 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Protein (human herpesvirus 6 strain U1102 gene U88) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Protein (human herpes virus 6 strain U1102 gene U88)
RN 167975-92-0 REGISTRY
SQL 413

L2 ANSWER 61 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Vicilin (Theobroma cacao clone pHD5P1.7 reduced) (9CI) (CA INDEX NAME)
RN 147388-33-8 REGISTRY
SQL 542

L2 ANSWER 62 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Vicilin, prepro- (Theobroma cacao clone pHD5P1.7 reduced) (9CI) (CA INDEX NAME)
RN 147388-32-7 REGISTRY
SQL 566

L2 ANSWER 63 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Vicilin, pro- (Theobroma cacao clone pMS600/pMS800 reduced) (9CI) (CA INDEX NAME)

RN 147095-05-4 REGISTRY
SQL 546

L2 ANSWER 64 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Protein (Drosophila melanogaster clone .lambda.Dm2.2 gene Mst84Dd reduced) (9CI) (CA INDEX NAME)
RN 144905-11-3 REGISTRY
SQL 68

L2 ANSWER 65 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Protein (Drosophila melanogaster clone .lambda.Dm2.2 gene Mst84Db reduced) (9CI) (CA INDEX NAME)
RN 144905-07-7 REGISTRY
SQL 74

L2 ANSWER 66 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Vicilin, prepro- (Theobroma cacao clone pMS600/pMS800 reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Protein, prepro- (Theobroma cacao clone pMS600/pMS800 49.0-kilodalton reduced)
RN 141961-55-9 REGISTRY
SQL 566

L2 ANSWER 67 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Protein UHS-SER 2 (mouse clone M16-8H reduced) (9CI) (CA INDEX NAME)
RN 132212-43-2 REGISTRY
SQL 223

L2 ANSWER 68 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Receptor, insulin, pro- (mouse clone pET-IR protein moiety reduced) (9CI) (CA INDEX NAME)
RN 126649-13-6 REGISTRY
SQL 1345

L2 ANSWER 69 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Vicilin B, pro- (cotton protein moiety reduced) (9CI) (CA INDEX NAME)
RN 113670-45-4 REGISTRY
SQL 565

L2 ANSWER 70 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Vicilin B, prepro- (cotton protein moiety reduced) (9CI) (CA INDEX NAME)
RN 113670-44-3 REGISTRY
SQL 590

L2 ANSWER 71 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Vicilin A, pro- (cotton reduced) (9CI) (CA INDEX NAME)
RN 113670-43-2 REGISTRY
SQL 580

L2 ANSWER 72 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Vicilin A, prepro- (cotton reduced) (9CI) (CA INDEX NAME)
RN 113670-42-1 REGISTRY
SQL 605

L2 ANSWER 73 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN Metallothionein (Drosophila melanogaster clone pCd2/pCd14 protein moiety reduced) (9CI) (CA INDEX NAME)
RN 109189-62-0 REGISTRY
SQL 43

L2 ANSWER 74 OF 75 REGISTRY COPYRIGHT 2000 ACS

CN .alpha.-Globulin, pro- (cotton clone C-72 protein moiety reduced) (9CI) (CA INDEX NAME)
RN 106388-00-5 REGISTRY
SQL 563

L2 ANSWER 75 OF 75 REGISTRY COPYRIGHT 2000 ACS
CN .alpha.-Globulin, prepro- (cotton clone C-72 protein moiety reduced) (9CI) (CA INDEX NAME)
RN 106387-99-9 REGISTRY
SQL 588

FILE 'CAPLUS' ENTERED AT 15:00:35 ON 11 MAY 2000
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FILE COVERS 1967 - 11 May 2000 VOL 132 ISS 20
FILE LAST UPDATED: 10 May 2000 (20000510/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

This file supports REGlstRY for direct browsing and searching of all substance data from the REGISTRY file. Enter HELP FIRST for more information.

Now you can extend your author, patent assignee, patent information, and title searches back to 1907. The records from 1907-1966 now have this searchable data in CAOLD. You now have electronic access to all of CA: 1907 to 1966 in CAOLD and 1967 to the present in CAPLUS on STN.

L2 75 SEA FILE=REGISTRY ABB=ON [YF]..C...C.{10-12}C...C...[YF]|C..C...C.{10-12}C...C...C/SQSP
L3 41 SEA FILE=CAPLUS ABB=ON L2

=> d ibib ab hitrn l3 1-41; fil hom

L3 ANSWER 1 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:246848 CAPLUS
TITLE: The genome sequence of Drosophila melanogaster
AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor;
Searched by Barb O'Bryen, STIC 308-4291

Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson, Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarry, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine; Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo, Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; et al.

CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA

SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195
CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The fly Drosophila melanogaster is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was detd. of nearly all of the .apprx.120-megabase euchromatic portion of the Drosophila genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller Caenorhabditis elegans genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBast at

http://flybase.bio.indiana.edu and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstr. record is one of 4 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT INDEXING IN PROGRESS

IT **263489-50-5 263489-51-6 263557-65-9 263557-66-0 263557-82-0**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of Drosophila melanogaster)

L3 ANSWER 2 OF 41 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 2000:246831 CAPLUS

TITLE: The genome sequence of Drosophila melanogaster

AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz De; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson, Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarry, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine;

Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo, Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; et al.
CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA
SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The fly Drosophila melanogaster is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was detd. of nearly all of the .apprx.120-megabase euchromatic portion of the Drosophila genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller Caenorhabditis elegans genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at http://flybase.bio.indiana.edu and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstr. record is one of 4 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].
IT **263104-93-4 263132-70-3**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of Drosophila melanogaster)

L3 ANSWER 3 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:164617 CAPLUS
DOCUMENT NUMBER: 132:218003
TITLE: Nucleic acids encoding human membrane-bound proteins and receptors
INVENTOR(S): Baker, Kevin; Goddard, Audrey; Gurney, Austin L.; Smith, Victoria; Watanabe, Colin K.; Wood, William I.
PATENT ASSIGNEE(S): Genentech, Inc., USA
SOURCE: PCT Int. Appl., 773 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000012708	A2	20000309	WO 1999-US20111	19990901

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,

CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:
US 1998-PV98716 19980901
US 1998-PV98749 19980901
US 1998-PV98750 19980901
US 1998-PV98803 19980902
US 1998-PV98821 19980902
US 1998-PV98843 19980902
US 1998-PV99536 19980909
US 1998-PV99596 19980909
US 1998-PV99598 19980909
US 1998-PV99602 19980909
US 1998-PV99642 19980909
US 1998-PV99741 19980910
US 1998-PV99754 19980910
US 1998-PV99763 19980910
US 1998-PV99792 19980910
US 1998-PV99808 19980910
US 1998-PV99812 19980910
US 1998-PV99815 19980910
US 1998-PV99816 19980910
US 1998-PV100385 19980915

AB Membrane-bound proteins and receptor mols. have various industrial applications, including as pharmaceutical and diagnostic agents. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins. The present invention is directed to 123 novel polypeptides and to nucleic acid mols. encoding those polypeptides identified in human cDNA libraries by (1) extracellular domain homol. screening, (2) amylase screening, or (3) signal algorithm anal. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide mols. comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

IT **260533-83-3P**
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(nucleotide sequence; nucleic acids encoding human membrane-bound proteins and receptors)

L3 ANSWER 4 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:145040 CAPLUS
DOCUMENT NUMBER: 132:204000
TITLE: Pig endogenous retrovirus envelope (PERV-D env) gene, detection of porcine retrovirus, and host immunization
INVENTOR(S): Banerjee, Papia T.; Patience, Clive; Andersson, Goran K.
PATENT ASSIGNEE(S): Bio-Transplant, Inc., USA
SOURCE: PCT Int. Appl., 119 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000011187	A1	20000302	WO 1999-US19053	19990818

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX,

NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,
UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.: US 1998-97015 19980818

AB Pig endogenous retrovirus envelope (PERV-D env) gene sequence, and its use in the detection of porcine retrovirus in tissue samples, a method of creating passive immunity in a host, and a vaccine and a method for immunizing a host against porcine retrovirus are disclosed. Antibodies, primers and probes for the above mentioned uses are also provided. A new pig endogenous retrovirus envelope (PERV-D env) gene was isolated and sequenced. Primers specific to the PERV-D env gene sequence were constructed and used to detect PERV-D in sample tissues in a PCR based method. The invention could be potentially useful in preventing the viral infection of organ transplant recipient, when the organ is of porcine origin.

IT **260383-93-5 260383-95-7**
RL: PRP (Properties)
(unclaimed protein sequence; pig endogenous retrovirus envelope (PERV-D env) gene, detection of porcine retrovirus, and host immunization)

L3 ANSWER 5 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:78873 CAPLUS
DOCUMENT NUMBER: 132:133209
TITLE: Humanized green fluorescent protein genes with preferred codon usage for expression in mammalian cells
INVENTOR(S): Muzyczka, Nicholas; Zolotukhin, Sergei; Hauswirth, William
PATENT ASSIGNEE(S): University of Florida, USA
SOURCE: U.S., 70 pp., Cont.-in-part of U.S. Ser. No. 588,201.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6020192	A	20000201	US 1997-893327	19970716
US 5874304	A	19990223	US 1996-588201	19960118
CA 2243088	AA	19970724	CA 1997-2243088	19970117
US 5968750	A	19991019	US 1998-169605	19981009

PRIORITY APPLN. INFO.: US 1996-588201 19960118

AB Disclosed are synthetic and "humanized" versions of green fluorescent protein (GFP) genes adapted for high level expression in mammalian cells, esp. those of human origin. Base substitutions are made in various codons in order to change the codon usage to one more appropriate for expression in mammalian cells. Also provided are variant or mutant GFP gene sequences, and a sequence of GFP gene fused with a nuclear targeting sequence, SV40 large T-antigen nuclear localization signal. Recombinant adeno-assocd. virus (AAV) vectors carrying such humanized genes are also disclosed. In addn., various methods for using the efficient expression of humanized GFP in mammalian cells and in animals are described.

IT **255704-94-0**
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; humanized green fluorescent protein genes with preferred codon usage for expression in mammalian cells)

L3 ANSWER 6 OF 41 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 2000:67509 CAPLUS
DOCUMENT NUMBER: 132:119024
TITLE: Peptides comprising repetitive units of amino acids and DNA sequences encoding the same for production of fibers for use in prosthetics
INVENTOR(S): Ferrari, Franco A.; Richardson, Charles; Chambers, James; Causey, Stuart; Pollock, Thomas J.; Cappello, Joseph; Crissman, John W.
PATENT ASSIGNEE(S): Protein Polymer Technologies, Inc., USA
SOURCE: U.S., 102 pp., Cont.-in-part of U.S. 5,641,648.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 16
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6018030	A	20000125	US 1995-482085	19950607
US 5243038	A	19930907	US 1987-114618	19871029
JP 10014586	A2	19980120	JP 1997-63870	19871029
US 5641648	A	19970624	US 1993-175155	19931229
PRIORITY APPLN. INFO.:			US 1986-927258	19861104
			US 1987-114618	19871029
			US 1993-53049	19930422
			US 1993-175155	19931229
			JP 1988-500640	19871029
			US 1988-269429	19881109
			US 1990-609716	19901106

AB Polypeptides comprising repetitive units of amino acids, as well as synthetic genes encoding the subject polypeptides are provided. The subject polypeptides are characterized by comprising repetitive units of amino acids, where the repetitive units are present in naturally occurring proteins, particularly naturally occurring structural proteins. The subject polypeptides find use in a variety of applications, such as structural components of prosthetic devices, synthetic fibers, and the like.

IT **255900-75-5**
RL: PRP (Properties)
(unclaimed protein sequence; peptides comprising repetitive units of amino acids and DNA sequences encoding the same for prodn. of fibers for use in prosthetics)

L3 ANSWER 7 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:733863 CAPLUS
DOCUMENT NUMBER: 131:347538
TITLE: Genetic sequences and proteins related to Alzheimer's disease
INVENTOR(S): St. George-Hyslop, Peter H.; Rommens, Johanna M.; Fraser, Paul E.
PATENT ASSIGNEE(S): The Hospital for Sick Children, HSC Research and Development Limited Partnership, Can.; The Governing Council of the University of Toronto
SOURCE: U.S., 131 pp., Cont.-in-part of U.S. Ser. No. 509,359.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

Searched by Barb O'Bryen, STIC 308-4291

US 5986054	A	19991116	US 1996-592541	19960126
CA 2219214	AA	19961031	CA 1996-2219214	19960429
CN 1188508	A	19980722	CN 1996-194902	19960429
WO 9727296	A1	19970731	WO 1997-CA51	19970127
W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG			
AU 9712992	A1	19970820	AU 1997-12992	19970127
EP 876483	A1	19981111	EP 1997-900531	19970127
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT, IE, LT, LV, FI, RO			
US 6020143	A	20000201	US 1997-888077	19970703
US 5840540	A	19981124	US 1997-967101	19971110
PRIORITY APPLN. INFO.:			US 1995-431048	19950428
			US 1995-496841	19950628
			US 1995-509359	19950731
			US 1996-592541	19960126
			US 1996-21672	19960705
			US 1996-21673	19960705
			US 1996-21700	19960712
			US 1996-29895	19961108
			US 1997-34590	19970102
			WO 1997-CA51	19970127

AB The present invention describes the identification, isolation and cloning of two human presenilin genes, PS-1 and PS-2, mutations in which lead to familial Alzheimer's disease. The Alzheimer's related membrane protein (ARMP) gene (or presenilin I (PSI)) gene was isolated, cloned and sequenced from within the AD3 region on chromosome 14q4.3. In addn., direct sequencing of RT-PCR products spanning this 3.0 kb cDNA transcript isolated from affected members of at least 8 large pedigrees linked to chromosome 14, has led to the discovery of missense mutations in each of these different pedigrees. These mutations are absent in normal chromosomes. Also identified are presenilin homolog genes in mice, Caenorhabditis elegans (SEL-12) and Drosophila melanogaster (DmPS). Transcripts and products of these genes are useful in detecting and diagnosing Alzheimer's disease, developing therapeutics for treatment of Alzheimer's disease, as well as the isolation and manuf. of the protein, and the constructions of transgenic animals expressing the mutant genes.

IT **250242-56-9P**
RL: ADV (Adverse effect, including toxicity); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(nucleotide sequence; genetic sequences and proteins related to Alzheimer's disease)

L3 ANSWER 8 OF 41 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER:	1999:717434 CAPLUS
DOCUMENT NUMBER:	132:248524
TITLE:	A family of antimicrobial peptides is produced by processing of a 7S globulin protein in Macadamia integrifolia kernels
AUTHOR(S):	Marcus, John P.; Green, Jodie L.; Goulter, Ken C.; Manners, John M.
CORPORATE SOURCE:	Cooperative Research Centre for Tropical Plant Pathology, The University of Queensland, Brisbane, 4072, Australia
SOURCE:	Plant J. (1999), 19(6), 699-710 Searched by Barb O'Bryen, STIC 308-4291

CODEN: PLJUED; ISSN: 0960-7412
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A new family of antimicrobial peptides has been discovered in Macadamia integrifolia. The first member of this new family to be purified from nut kernels was a peptide of 45 amino acid (aa) residues, termed MiAMP2c. This peptide inhibited various plant pathogenic fungi in vitro. CDNA clones corresponding to MiAMP2c encoded a 666 aa precursor protein homologous to vicilin 7S globulin proteins. The deduced precursor protein sequence contained a putative hydrophobic N-terminal signal sequence (28 aa), an extremely hydrophilic N-proximal region (212 aa), and a C-terminal region of 426 aa which is represented in all vicilins. The hydrophilic portion of the deduced protein contained the sequence for MiAMP2c as well as three addnl. segments having the same cysteine spacing pattern as MiAMP2c. Each member of the MiAMP2 family (i.e. MiAMP2a, b, c and d) consisted of approx. 50 amino acids and contained a C-X-X-X-C-(10-12)X-C-X-X-X-C motif. Subsequent isolations from seed exudates led to the purifn. of the predicted family members MiAMP2b and 2d, both of which also exhibited antimicrobial activity in vitro. These results suggest that some vicilins play a role in defense during seed germination.

IT **262433-66-9P 262433-70-5P 262433-71-6P**
262434-56-0P
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); PRP (Properties); PUR (Purification or recovery); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(amino acid sequence; family of antimicrobial peptides is produced by processing of a 7S globulin protein in Macadamia integrifolia kernels)

IT **209902-50-1 209902-52-3 209902-56-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; family of antimicrobial peptides is produced by processing of a 7S globulin protein in Macadamia integrifolia kernels)

L3 ANSWER 9 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:691234 CAPLUS
DOCUMENT NUMBER: 131:333021
TITLE: Solanum tuberosum-derived viral resistance gene which induces cell death and extreme and hypervariable resistance
INVENTOR(S): Bendahmane, Abdelhafid; Baulcombe, David Charles; Kanyuka, Konstantin Valerievich
PATENT ASSIGNEE(S): Plant Bioscience Limited, UK
SOURCE: PCT Int. Appl., 124 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9954490	A2	19991028	WO 1999-GB1182	19990416
WO 9954490	A3	20000106		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,

CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9935296	A1	19991108	AU 1999-35296	19990416
PRIORITY APPLN. INFO.:			GB 1998-8083	19980416
			WO 1999-GB1182	19990416

AB Disclosed are nucleic acids encoding polypeptides which are capable of conferring extreme resistance (ER) against, and being triggered by, plant pathogens such as viruses (e.g. PVX and related isolates). Preferred nucleic acids encode the Rx polynucleotide from Solanum tuberosum , or a variety of homologues (naturally occurring or derivs.) thereof, such as 111h1; 221h2; Ac15; Ac64; K39.hom. Rx is a resistance gene from potato conferring extreme resistance against potato virus X. In addn. it gives resistance to Potex and Carlaviruses. It is able to induce cell death in some cells of leaves and thus lead to systemic acquired resistance against different pathogens. Rx genes are widely applicable in breeding programs because Rx is highly durable with only one natural isolate able to overcome the resistance and the resistance is extreme. Rx-mediated resistance is active in protoplasts where it suppresses viral replication or promotes degrdn. of viral RNA. Particular methods of activating resistance by using combinations of resistance gene and elicitor are also disclosed, which in certain cases lead to a hypersensitive response. This hypersensitive response is a secondary resistance response involving decoupled continuous activation of Rx by the 35S viral coat protein. Further aspects of the invention include specific primers, vectors, host cells, polypeptides, antibodies and transgenic plants, plus methods of producing and employing these, in particular for influencing a resistance trait in a plant.

IT **249577-36-4 249577-38-6 249577-41-1**
249577-44-4 249577-46-6
RL: AGR (Agricultural use); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; solanum tuberosum-derived viral resistance gene which induces cell death and extreme and hypervariable resistance)

IT **249569-19-5**, PN: WO9954490 FIG: 7A unclaimed protein
RL: PRP (Properties)
(unclaimed protein sequence; solanum tuberosum-derived viral resistance gene which induces cell death and extreme and hypervariable resistance)

IT **249569-21-9**
RL: PRP (Properties)
(unclaimed sequence; solanum tuberosum-derived viral resistance gene which induces cell death and extreme and hypervariable resistance)

L3 ANSWER 10 OF 41 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER:	1999:691206 CAPLUS
DOCUMENT NUMBER:	131:333014
TITLE:	Human bladder nucleic acid sequences and proteins and their use in drug screening and bladder tumor inhibition
INVENTOR(S):	Specht, Thomas; Hinzmann, Bernd; Schmitt, Armin; Pilarsky, Christian; Dahl, Edgar; Rosenthal, Andre
PATENT ASSIGNEE(S):	Metagen Gesellschaft fur Genomforschung mbH, Germany
SOURCE:	PCT Int. Appl., 355 pp. CODEN: PIXXD2
DOCUMENT TYPE:	Patent
LANGUAGE:	German
FAMILY ACC. NUM. COUNT:	1
PATENT INFORMATION:	

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9954460	A2	19991028	WO 1999-DE1163	19990415
W: JP, US				

Searched by Barb O'Bryen, STIC 308-4291

RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

DE 19818620 A1 19991028 DE 1998-19818620 19980421

PRIORITY APPLN. INFO.: DE 1998-19818620 19980421

AB The invention relates to human nucleic acid sequences (mRNA, cDNA, genomic sequences) of normal bladder tissue, coding for proteins or parts thereof, in addn. to the use thereof. The invention also relates to the proteins that can be obtained according to said sequences and to the use thereof. Thus, through computer anal. of EST databanks and electronic Northern blotting, cDNAs characteristic of human bladder tissue were identified.

IT **249906-26-1P**, Protein (human bladder fragment)
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; human bladder nucleic acid sequences and proteins and their use in drug screening and bladder tumor inhibition)

L3 ANSWER 11 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:691187 CAPLUS
DOCUMENT NUMBER: 131:333013
TITLE: Insulin-like proteins and nucleic acids of Caenorhabditis elegans
INVENTOR(S): Homburger, Sheila A.; Platt, Darren M.; Ferguson, Kimberly C.; Doberstein, Stephen K.; Buchman, Andrew R.; Reddy, Bindu P.
PATENT ASSIGNEE(S): Exelixis Pharmaceuticals, Inc., USA
SOURCE: PCT Int. Appl., 194 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9954436	A2	19991028	WO 1999-US8522	19990416
WO 9954436	A3	19991229		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1998-62580 19980417
US 1998-74984 19980508
US 1998-84303 19980526

AB The present invention relates to Caenorhabditis elegans insulin-like genes and methods for identifying insulin-like genes. The methods provide nucleotide sequences of C. elegans insulin-like genes, amino acid sequences of their encoded proteins, and derivs. (e.g., fragments) and analogs thereof. Thus, at least 31 insulin-like genes are identified, and the structure and expression of the coding regions of 22 of these putative C. elegans insulin-like genes were confirmed using an exptl. approach involving reverse transcription of C. elegans mRNA, PCR amplification of specific cDNAs, cloning, and DNA sequencing. The invention further relates to fragments (and derivs. and analogs thereof) of insulin-like proteins which comprise one or more domains of an insulin-like protein. Antibodies to an insulin-like protein, and derivs. and analogs thereof,

are provided. Methods of prodn. of an insulin-like protein (e.g., by recombinant means), and derivs. and analogs thereof, are provided. Further, methods to identify the biol. function of a C. elegans insulin-like gene are provided, including various methods for the functional modification (e.g., overexpression, underexpression, mutation, knock-out) of one or more genes simultaneously. Still further, methods to identify a C. elegans gene which modifies the function of, and/or functions in a downstream pathway from, an insulin-like gene are provided.

IT **207465-94-9DP**, subfragments are claimed
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; insulin-like proteins and nucleic acids of Caenorhabditis elegans)

L3 ANSWER 12 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:686627 CAPLUS
DOCUMENT NUMBER: 131:319671
TITLE: Cloning, expression, sequence and possible therapeutic use of human carbonic anhydrase VIII
INVENTOR(S): Bandman, Olga; Yue, Henry; Greenwald, Sara R.; Corley, Neil C.
PATENT ASSIGNEE(S): Incyte Pharmaceuticals, Inc., USA
SOURCE: U.S., 38 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5972684	A	19991026	US 1997-977767	19971125

AB The invention provides a human carbonic anhydrase isoform (CAVIII) and polynucleotides which identify and encode CAVIII. Nucleic acids encoding CAVIII were first identified in Incyte clone 2059155 from a cDNA library using a computer search for amino acid sequence alignments; a consensus sequence was derived from overlapping and/or extended nucleic acid sequences. Amino acid and cDNA sequences for CAVIII are reported. CAVIII is 328 amino acids in length. Expression of CAVIII has been shown and the enzyme activity has been demonstrated. Naturally occurring CAVIII has been purified using specific antibodies. The invention also provides expression vectors, host cells, agonists, antibodies and antagonists. The invention also provides methods for treating disorders assocd. with expression of CAVIII.

IT **249299-76-1**, PN: US5972684 SEQID: 3 unclaimed protein
RL: PRP (Properties)
(unclaimed protein sequence; cloning, expression, sequence and possible therapeutic use of human carbonic anhydrase VIII)

L3 ANSWER 13 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:673017 CAPLUS
DOCUMENT NUMBER: 131:307686
TITLE: 5'-Expressed sequence tags for secreted proteins identified from human tissues
INVENTOR(S): Dumas Milne Edwards, Jean-Baptiste; Duclert, Aymeric; Giordano, Jean-Yves
PATENT ASSIGNEE(S): Genset S. A., Fr.
SOURCE: PCT Int. Appl., 837 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
Searched by Barb O'Bryen, STIC 308-4291

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9953051	A2	19991021	WO 1999-IB712	19990409
W: AU, CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9930501	A1	19991101	AU 1999-30501	19990409
PRIORITY APPLN. INFO.:			US 1998-57719	19980409
			US 1998-69047	19980428
			WO 1999-IB712	19990409

AB The sequences of the 5' ends of 788 expressed sequence tags (ESTs) derived from mRNAs encoding human secreted proteins are disclosed. Chem. and enzymic methods of obtaining mRNAs with intact 5' ends, computer anal. of the isolated 5' ESTs, generation of consensus contigated 5' ESTs, and identification of open reading frames and potential signal sequences are described. Total human RNA or poly(A)+ RNAs derived from 29 different tissues were purchased from LABIMO and CLONTECH and used to generate 44 cDNA libraries. Prepns. of mRNAs with <5% of rRNA and uncontaminated by exogenous sequences (prokaryotic or fungal) were used in library construction. Seven hundred five of the nucleic acids have an incomplete ORF which encodes a signal peptide, 47 have an incomplete ORF in which no sequence encoding a signal peptide has been identified, 27 have a complete ORF which encodes a signal peptide, and 19 have a complete ORF in which no sequence encoding a signal peptide has been identified. Tissue of origin and spatial and temporal tissue expression patterns of mRNAs corresponding to each of the 5' ESTs are also provided. The 5' ESTs may be to obtain cDNAS, and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.

IT **247017-76-1P**
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; 5'-ends of expressed sequence tags for secreted proteins from human tissues)

L3 ANSWER 14 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:659510 CAPLUS
DOCUMENT NUMBER: 131:296204
TITLE: Fusion proteins of Mycobacterium tuberculosis antigens containing domains from more than one Mycobacterium protein and their uses
INVENTOR(S): Skeiky, Yasir A. W.; Alderson, Mark; Campos-Neto, Antonio
PATENT ASSIGNEE(S): Corixa Corporation, USA
SOURCE: PCT Int. Appl., 83 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9951748	A2	19991014	WO 1999-US7717	19990407
WO 2000051748	A3	20000203		
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK,				

MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9934817	A1	19991025	AU 1999-34817	19990407
PRIORITY APPLN. INFO.:			US 1998-56556	19980407
			US 1998-223040	19981230
			WO 1999-US7717	19990407

AB Fusion proteins contg. antigenic regions from two or more proteins (up to five) of Mycobacterium tuberculosis that can be used in the diagnosis, treatment and prevention of tuberculosis infection are described. These fusion proteins retain the antigenicity of the originals. A series of twelve fusion proteins contg. combinations of peptides from M. tuberculosis antigens were constructed by std. methods and manufd. as inclusion bodies in Escherichia coli. The fusion proteins stimulated T cell proliferation in PPD+ patients with proliferation patterns similar to those of the individual components. Immunization of mice with the fusion proteins induced strong interferon .gamma. and interleukin 4 responses with the strength of the responses depending upon the adjuvant used.

IT **246852-79-9**
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; fusion proteins of Mycobacterium tuberculosis antigens contg. domains from more than one Mycobacterium protein and their uses)

L3 ANSWER 15 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:659492 CAPLUS
DOCUMENT NUMBER: 131:282417
TITLE: Control of floral induction in plants with maize Id gene and methods for identification of zinc-finger proteins and producing alternative alleles
INVENTOR(S): Colasanti, Joseph J.; Sundaresan, Venkatesan
PATENT ASSIGNEE(S): Cold Spring Harbor Laboratory, USA
SOURCE: PCT Int. Appl., 81 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9951728	A2	19991014	WO 1999-US7157	19990331
WO 9951728	A3	19991118		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9934610	A1	19991025	AU 1999-34610	19990331
PRIORITY APPLN. INFO.:			US 1998-56226	19980407
			WO 1999-US7157	19990331

AB The Id gene which controls flower evocation in maize plants is described. The maize nucleic acid is similar to that of genes encoding zinc-finger regulatory proteins in animals. Methods of isolation or prepn. of other

regulatory protein genes in plants and their uses are disclosed. In addn. this paper provides a means to eliminate the need for detasseling in the prodn. of maize and sorghum hybrids.

IT **246036-79-3**, PN: WO9951728 SEQID: 4 unclaimed protein
RL: PRP (Properties)
(unclaimed protein sequence; control of floral induction in plants with maize Id gene and methods for identification of zinc-finger proteins and producing alternative alleles)

L3 ANSWER 16 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:513698 CAPLUS
DOCUMENT NUMBER: 132:219312
TITLE: Genetic analysis of Porphyromonas gingivalis fimbria-deficient mutant: involvement of a two-component signal transduction system for fimbriation
AUTHOR(S): Hayashi, Jun-Ichiro
CORPORATE SOURCE: Department of Periodontlogy, School of Dentistry, Aichi-Gakuin University, Japan
SOURCE: Aichi Gakuin Daigaku Shigakkaishi (1999), 37(1), 219-232
CODEN: AGDSAB; ISSN: 0044-6912
PUBLISHER: Aichi Gakuin Daigaku Shigakkai
DOCUMENT TYPE: Journal
LANGUAGE: Japanese

AB Porphyromonas gingivalis, a gram-neg. black-pigmented anaerobe, has been implicated as one of the pathogens in adult periodontitis. The majority of P. gingivalis strains have fimbriae that are considered to be an important virulence factor of this organism because of their adherent functions. Recently, 22 fimbria-deficient mutants were isolated by transposon mutagenesis using Tn4351 and 8 of them have been shown to have insertion of Tn4351 somewhere in or about the 300-kbp NotI fragment, about 200-kbp away from the fimA gene. In order to elucidate the insertion loci, these 8 mutants were analyzed by Southern hybridization using a Tn4351-specific probe. Since 4 of them were inserted in a specific region, an 8-kbp PvuII-AccI fragment carrying Tn4351 was cloned from one of the 4 mutants, AG30-4. Sequencing of flanking regions (2.3 kbp) was carried out. From the sequence data, an ORF interrupted by Tn4351 was found in the fragment. A homol. search of the gene databases and unfinished P. gingivalis W83 genome sequence using the BLAST program revealed that a gene product of the ORF, with about 240 conserved amino acid residues in the C-terminus, was a homolog of sensor histidine kinase in bacteria. Also, there seemed to be another ORF downstream from the sensor gene, which was a regulatory gene. The 2 close genes compose a so-called two-component signal transduction system in bacteria. Furthermore, the rest of the mutants were analyzed for the exact mutation sites. Five mutants had insertions in the sensor gene and 2 mutants in the putative regulatory gene. These observations suggest that a two-component system in P. gingivalis is involved in fimbriation.

IT **260773-72-6**
RL: BPR (Biological process); PRP (Properties); BIOL (Biological study); PROC (Process)
(nucleotide sequence; involvement of a two-component signal transduction system for fimbriation in Porphyromonas gingivalis)

L3 ANSWER 17 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:495315 CAPLUS
DOCUMENT NUMBER: 131:139951
TITLE: Erythropoietin mutants with altered biological activity
INVENTOR(S): Sytkowski, Arthur J.; Grodberg, Jennifer
PATENT ASSIGNEE(S): Beth Israel Deaconess Medical Center, USA
Searched by Barb O'Bryen, STIC 308-4291

SOURCE: PCT Int. Appl., 106 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9938890	A1	19990805	WO 1999-US2258	19990202
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9925766	A1	19990816	AU 1999-25766	19990202
PRIORITY APPLN. INFO.:			US 1998-17631	19980203
			WO 1999-US2258	19990202

AB The invention relates to DNA encoding modified, secretable erythropoietin proteins whose ability to regulate the growth and differentiation of red blood cell progenitors are different from the wild-type recombinant erythropoietin. The invention also relates to methods of modifying or altering the regulating activity of the secretable erythropoietin proteins and the use of the modified secretable erythropoietin proteins, for example, in in vivo therapeutics. Thus, oligonucleotide-directed mutagenesis was used to create mutant erythropoietin which resulted in substitution of amino acids at positions 100-109 within Domain 1. Arginine-103 was crit. for erythropoietin's biol. activity, and serine-104, leucine-105, and leucine-108 appear to play a role, as indicated by the decreased biol. activity of these mutants. Some of the mutant erythropoietin proteins demonstrated increased heat stability relative to the wild-type erythropoietin protein. Alterations in the noncoding regions of the erythropoietin gene can affect mRNA stability, rates of translation, expression from host cells, protein processing, export from rough endoplasmic reticulum, extend and pattern of glycosylation, secretion dynamics and rate of export from the cell. The free energy for mRNA secondary structure for nucleotides 401-624 in the 5'-untranslated region of the erythropoietin gene is predicted to be -161.0 kcal/mol, and deletions in this area decrease the free energy values; similar changes in free energy are obsd for nucleotides 2773-2972 in the 3'-untranslated region. Erythropoietin mutants with modified biol. activities may be of use to treat anemia.

IT **234439-19-1**
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(mutants in 5'- and 3'-UTR regions; erythropoietin mutants with altered biol. activity)

L3 ANSWER 18 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:390388 CAPLUS
DOCUMENT NUMBER: 131:40577
TITLE: Characterization and cDNA sequence for CtIP, a novel human protein that interacts with CtBP
INVENTOR(S): Chinnadurai, Govindaswamy
PATENT ASSIGNEE(S): Saint Louis University, USA
SOURCE: PCT Int. Appl., 45 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
Searched by Barb O'Bryen, STIC 308-4291

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9929334	A1	19990617	WO 1998-US26505	19981211
W: AU, CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9918224	A1	19990628	AU 1999-18224	19981211
PRIORITY APPLN. INFO.:			US 1997-69362	19971212
			US 1997-PV69362	19971212
			WO 1998-US26505	19981211

AB A novel human protein, CtIP (CtBP-Interacting Protein), that binds the human cellular protein CtBP (E1A C-terminal Binding Protein), and the cDNA sequence encoding CtIP are provided. Said protein binds with CtBP via the same five amino acid motif (PLDLS) found in adenovirus E1A proteins, and this binding is disrupted by E1A proteins and/or deletion of the binding motif. As the CtBP-binding region of E1A has been implicated in transcriptional regulatory activity, it is believed that CtIP has a transcriptional regulatory activity that plays a role in the obsd. oncogenesis-restraining activity of the C-terminal region of E1A proteins. Thus, CtIP is useful in diagnostic methods for detg. malignancy of cells and for identifying agents that can inhibit neoplasia.

IT **227188-49-0**
RL: BOC (Biological occurrence); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; characterization and cDNA sequence for CtIP, a novel human protein that interacts with CtBP)

L3 ANSWER 19 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:189197 CAPLUS
DOCUMENT NUMBER: 130:232471
TITLE: The protein conductin and its application for diagnosis and gene therapy of colon cancer
INVENTOR(S): Behrens, Jurgen; Birchmeier, Walter
PATENT ASSIGNEE(S): Max-Delbruck-Centrum fur Molekulare Medizin, Germany
SOURCE: PCT Int. Appl., 22 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9911780	A2	19990311	WO 1998-DE2621	19980901
WO 9911780	A3	19990527		
W: CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
DE 19840875	A1	19990512	DE 1998-19840875	19980901
PRIORITY APPLN. INFO.:			DE 1997-19738205	19970902

AB The invention concerns the novel protein conductin that is able to regulate the .beta.-catenin function and interacts with the tumor suppressor adenomatous polyposis coli (APC); and its application in the gene therapy of colon cancer. The 840 amino acid contg. protein contains domains with various activities: 78-200 is the RGS (Regulator of G-Protein Signalling) binding sequence; 343-396 is the GSK 3.beta. (glycogen synthase kinase 3.beta.) binding sequence; 397-465 is the .beta.-catenin binding sequence; 783-833 is the Dishevelled homol. region. Mutations,

variants and fragments of conductin with the corresponding coding genes and mRNA sequences are also included. Antibodies and nucleic acid probes for the detection of conductin are part of the diagnosis tools. For therapeutic purposes a vector contg. the conductin gene is constructed; substances that activate and reactivate conductin in the body are co-administered, e.g. a substance that activates the conductin promoter or stabilizes mRNA. The effect of conductin was proved using SW480 cells with APC mutation and thus increased .beta.-catenin level. Introduction of conductin resulted in the decrease of .beta.-catenin to the same concn. as in non APC mutated SW480 cells. In an expt. with Xenopus embryos it was shown that conductin inhibits the Wnt/Wingless signaling pathway via its interaction with .beta.-catenin.

IT **221220-54-8**
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; protein conductin and application for diagnosis and gene therapy of colon cancer)

L3 ANSWER 20 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:166633 CAPLUS
DOCUMENT NUMBER: 130:219154
TITLE: DNA molecules encoding human nuclear receptor proteins
INVENTOR(S): Chen, Fang
PATENT ASSIGNEE(S): Merck & Co., Inc., USA
SOURCE: PCT Int. Appl., 82 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9910367	A1	19990304	WO 1998-US17826	19980827
W: CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6054295	A	20000425	US 1998-141000	19980826
PRIORITY APPLN. INFO.:			US 1997-PV57090	19970827
			US 1997-PV62902	19971021
			US 1998-PV78633	19980319

AB The present invention discloses the isolation and characterization of cDNA mols. encoding two human nuclear receptor proteins, designated nNR1, nNR2 and/or nNR2-1. The nNR1 and nNR2 proteins share 95 and 77% homol. at the amino acid level to hERR2. The gene encoding nNR1 is located on locus 14q24.3-14q31, which is the Alzheimer disease gene 3 (AD3) locus. An alternative form of cDNA encoding nNR2 contains a 2-nucleotide insertion at nucleotide 1352, resulting in shifted reading frame and introduction of a TGA termination codon 33 nucleotides from the insertion site and thus a C-terminal truncated nNR2, nNR2-1. Also within the scope of the disclosure are recombinant vectors, recombinant host cells, methods of screening for modulators of nNR1, nNR2 and/or nNR2-1 activity, and prodn. of antibodies against nNR1, nNR2 and/or nNR2-1, or epitopes thereof.

IT **221111-80-4**, DNA (human nuclear receptor nNR2 cDNA)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; DNA mols. encoding human nuclear receptor proteins)

L3 ANSWER 21 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:8025 CAPLUS
DOCUMENT NUMBER: 130:62689
Searched by Barb O'Bryen, STIC 308-4291

TITLE: sequence and therapeutic applications for human Hm74a receptor isoform
INVENTOR(S): Elshourbagy, Nabil A.; Li, Xiaotong; Bergsma, Derk J.; Mooney, Jeffrey L.; Guerrera, Stephanie F.
PATENT ASSIGNEE(S): Smithkline Beecham Corporation, USA
SOURCE: PCT Int. Appl., 40 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9856820	A1	19981217	WO 1998-US12386	19980612
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9879660	A1	19981230	AU 1998-79660	19980612
PRIORITY APPLN. INFO.:			US 1997-49480	19970612
			WO 1998-US12386	19980612

AB HM74A polypeptides and polynucleotides and methods for producing such polypeptides by recombinant techniques are disclosed. Also disclosed are methods for utilizing HM74A polypeptides and polynucleotides in therapy, and diagnostic assays for such. Therapeutic applications include treatment for bacterial or protozoan or fungal or viral infections. Specifically HIV-1, HIV-2, pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurol. mental disorders, anxiety , schizophrenia, manic depression, depression, delirium, dementia, severe mental retardation, dyskinesias, Huntingtons disease and Gilles dela Tourett's syndrome are treatable with this peptide.

IT **217945-23-8**
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; sequence and therapeutic applications for human Hm74a receptor isoform)

L3 ANSWER 22 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1998:674618 CAPLUS
DOCUMENT NUMBER: 130:1778
TITLE: Cloning of cDNA for a human GTPase activating protein (GAP) specific for the Rab3 subfamily of small G proteins
INVENTOR(S): Takai, Yoshimi
PATENT ASSIGNEE(S): Eisai Co., Ltd., Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 16 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

JP 10276783 A2 19981020 JP 1997-90706 19970409

AB The cDNA encoding a human GTPase activating protein (GAP) specific for the lipid-modified Rab3 subfamily of small G proteins, or Rab3GAP, is isolated from a human brain cDNA library. Expression of the cDNA in Escherichia coli is also obsd.

IT **215728-51-1**
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; cloning of cDNA for a human GTPase activating protein (GAP) specific for Rab3 subfamily of small G proteins)

L3 ANSWER 23 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1998:479359 CAPLUS
DOCUMENT NUMBER: 129:106487
TITLE: Antimicrobial protein MiAMP2c from Macadamia integrifolia and other plants
INVENTOR(S): Manners, John Michael; Marcus, John Paul; Goulter, Kenneth Clifford; Green, Jodie Lyn; Bower, Neil Ivan
PATENT ASSIGNEE(S): Cooperative Research Centre for Tropical Plant Pathology, Australia
SOURCE: PCT Int. Appl., 96 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9827805	A1	19980702	WO 1997-AU874	19971222
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9878697	A1	19980717	AU 1998-78697	19971222
PRIORITY APPLN. INFO.:			AU 1996-4275	19961220
			WO 1997-AU874	19971222

AB A new family of antimicrobial proteins is described. Prototype proteins are provided from Macadamia integrifolia (MiAMP2c) as well as other plant species. DNA encoding the proteins is also described as well as DNA constructs which can be used to express the antimicrobial protein or to introduce the antimicrobial protein into a plant. Compns. comprising the antimicrobial proteins or the antimicrobial protein per se can be administered to plants or mammalian animals to combat microbial infestation.

IT **209902-50-1P 209902-52-3P 209902-56-7P**
209902-58-9P 209902-59-0P, Antimicrobial protein GhAMP1 (cotton) **209909-54-6P 209909-55-7P**
209909-56-8P 209909-57-9P 209909-58-0P
209909-59-1P 209909-60-4P 209909-68-2P
209909-71-7P 209909-72-8P 209909-73-9P
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; antimicrobial protein MiAMP2c from Macadamia integrifolia and other plants)

L3 ANSWER 24 OF 41 CAPLUS COPYRIGHT 2000 ACS
Searched by Barb O'Bryen, STIC 308-4291

ACCESSION NUMBER: 1998:472384 CAPLUS
DOCUMENT NUMBER: 129:104912
TITLE: Complete genome sequence of Treponema pallidum, the syphilis spirochete
AUTHOR(S): Fraser, Claire M.; Norris, Steven J.; Weinstock, George M.; White, Owen; Sutton, Granger G.; Dodson, Robert; Gwinn, Michelle; Hickey, Erin K.; Clayton, Rebecca; Ketchum, Karen A.; Sodergren, Erica; Hardham, John M.; McLeod, Michael P.; Salzberg, Steven; Peterson, Jeremy; Khalak, Hanif; Richardson, Delwood; Howell, Jerrilyn K.; Chidambaram, Monjula; Utterback, Teresa; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Cotton, Matthew D.; Fujii, Claire; Garland, Stacey; Hatch, Bonnie; Horst, Kurt; Roberts, Kevin; Sandusky, Mina; Weidman, Janice; Smith, Hamilton O.; Venter, J. Craig
CORPORATE SOURCE: The Inst. Genomic Res., Rockville, MD, 20850, USA
SOURCE: Science (Washington, D. C.) (1998), 281(5375), 375-388
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The complete genome sequence of Treponema pallidum was detd. and shown to be 1,138,006 base pairs contg. 1041 predicted coding sequences (open reading frames). Systems for DNA replication, transcription, translation, and repair are intact, but catabolic and biosynthetic activities are minimized. The no. of identifiable transporters is small, and no phosphoenolpyruvate:phosphotransferase carbohydrate transporters were found. Potential virulence factors include a family of 12 potential membrane proteins and several putative hemolysins. Comparison of the T. pallidum genome sequence with that of another pathogenic spirochete, Borrelia burgdorferi, the agent of Lyme disease, identified unique and common genes and substantiates the considerable diversity obsd. among pathogenic spirochetes.
IT **209611-36-9**, Protein (Treponema pallidum gene TP0856)
RL: PRP (Properties)
(amino acid sequence; complete genome sequence of Treponema pallidum)

L3 ANSWER 25 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1998:394053 CAPLUS
DOCUMENT NUMBER: 129:94523
TITLE: Recombinant preparation of carotenoids using enzymes from Flavobacterium or gram-negative bacteria strain E-396 for feed or food industries
INVENTOR(S): Pasamontes, Luis; Tosigonkov, Juri
PATENT ASSIGNEE(S): F. Hoffmann-La Roche A.-G., Switz.
SOURCE: Jpn. Kokai Tokkyo Koho, 80 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 10155497	A2	19980616	JP 1997-348653	19971202
EP 872554	A2	19981021	EP 1997-120324	19971120
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
BR 9705676	A	19990525	BR 1997-5676	19971201
CN 1184159	A	19980610	CN 1997-122604	19971202

PRIORITY APPLN. INFO.: EP 1996-810839 19961202
Searched by Barb O'Bryen, STIC 308-4291

AB Disclosed is a method for industrial-scale prodn. of carotenoids by expression of the Flavobacterium strain R1534- or gram-neg. bacteria strain E-396-derived genes that are assocd. with the carotenoids-biosynthesis in a transgenic host such as Escherichia coli or Bacillus subtilis. The genes involved are crtE (for geranylgeranyl pyrophosphate synthetase), crtB (phytoene synthetase), crtI (phytoene desaturase), crtY (lycopene cyclase), all from Flavobacterium strain R1534, and crtZE396 (.beta.-carotene oxygenase) from gram-neg. bacteria strain E-396. Gene crtW encoding .beta.-carotene .beta.4-oxygenase of Alcaligenes strain PC-1 may also be used to improve the carotenoids prodn. Methods for fermn. prodn. of cantaxanthin, astaxanthin, adonixanthin, and zeaxanthin are claimed. Methods using genes crtEE396, crtBE396, crtIE396, crtYE396, crtZE396, and crtWE396, all from gram-neg. bacteria strain E-396, also claimed. Use of carotenoids as food or feed additives is also claimed.

IT **209540-17-0 209540-18-1**
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; recombinant prepn. of carotenoids using Flavobacterium or gram-neg. bacteria strain E-396 genes for feed or food industries)

L3 ANSWER 26 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1998:290843 CAPLUS
DOCUMENT NUMBER: 129:1234
TITLE: New insulin-like proteins with atypical disulfide bond pattern characterized in Caenorhabditis elegans by comparative sequence analysis and homology modeling
AUTHOR(S): Duret, Laurent; Guex, Nicolas; Peitsch, Manuel C.; Bairoch, Amos
CORPORATE SOURCE: Lab. BGBP-UMR Centre National de la Recherche Scientifique (CNRS), Univ. Claude Bernard, Villeurbanne, F-69622, Fr.
SOURCE: Genome Res. (1998), 8(4), 348-353
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We have identified three new families of insulin homologs in Caenorhabditis elegans. In two of these families, concerted mutations suggest that an addnl. disulfide bond links B and A domains, and that the A-domain internal disulfide bond is substituted by a hydrophobic interaction. Homol. modeling remarkably confirms these predictions and shows that despite this atypical disulfide bond pattern and the absence of C-like peptide, all these proteins may adopt the same fold as the insulin. Interestingly, whereas we identified 10 insulin-like peptides, only one insulin-like-receptor (daf-2) has been found. We propose that these insulin-related peptides may correspond to different activators or inhibitors of the daf-2 insulin-regulating pathway.

IT **207465-94-9**
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(insulin-like proteins with atypical disulfide bond pattern characterized in Caenorhabditis elegans by comparative sequence anal. and homol. modeling)

L3 ANSWER 27 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1997:634275 CAPLUS
DOCUMENT NUMBER: 127:327167
TITLE: Conservation of the H-2 BF1 binding motif 5' of the H-2Ds, Ks and Dq genes
AUTHOR(S): Brown, G. D.; Morris, D. R.; Meruelo, D.
CORPORATE SOURCE: Department of Pathology and Kaplan Cancer Centre, New

York University Medical Centre, New York, NY, USA
SOURCE: Eur. J. Immunogenet. (1997), 24(4), 241-257
CODEN: EJOIE3; ISSN: 0960-7420
PUBLISHER: Blackwell
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The biol. consequences of radiation leukemia virus (RadLV) infection include the stimulation of H-2 antigen expression soon after injection of the virus. Early studies demonstrated that resistance to RadLV-induced leukemia in certain mouse strains is mediated by genes in the H-2D region of the major histocompatibility complex (MHC). Recent studies have shown that elevated H-2D regions of the major histocompatibility complex (MHC). Recent studies have shown that elevated H-2Dd expression on the thymocyte cell surface of resistant mouse strains results from increased mRNA transcription and is correlated with elevated levels of a DNA-binding activity that recognizes a short DNA sequence 5' of the start of transcription for the H-2Dd gene. This binding activity has been termed H-2 binding factor 1 (H-2 BF1) and is found exclusively in the thymus. In an effort to examinethe H-2 genes of RadLV-susceptible mice for the presence of the H-2 BF1 binding target, we have clones class I genes from the highly susceptible B10.S mouse strain and have identified both the Ds and the Ks genes. The entire genomic sequence for the Ds gene has been detd. and is reported here. In addn., the 5' regulatory region of the previously cloned Dq gene has been sequenced; mice of the Dq haplotype are also susceptible to RadLV-induced leukemia. In this report, we show that the H-2 BF1 DNA binding sequence is present 5' of each of these three class I genes.

IT **197981-22-9**
RL: PRP (Properties)
(nucleotide sequence; conservation of the H-2 BF1 binding motif 5' of the H-2Ds, Ks and Dq genes)

L3 ANSWER 28 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1997:212344 CAPLUS
DOCUMENT NUMBER: 126:273049
TITLE: Molecular cloning and sequence analysis of a gene encoding rice proteinase inhibitor
AUTHOR(S): Xie, Ming; Chen, Xin; Qu, Lijia; Liu, Hong; Gu, Hongya; Chen, Zhanliang
CORPORATE SOURCE: State Key Lab. Protein Engineering & Plant Genetic Engineering, Beijing Univ., Beijing, 100871, Peop. Rep. China
SOURCE: Zhiwu Xuebao (1996), 38(6), 444-450
CODEN: CHWHAY; ISSN: 0577-7496
PUBLISHER: Kexue
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

AB With the primers designed basing on the terminal amino acid sequences of rice proteinase inhibitor and the preferred codons of rice genes, a new gene coding for a rice proteinase inhibitor was amplified and cloned from Oryza sativa var. japonica (cv. Zhonghua 8) using PCR technique. The gene contains 408 base-pairs and encodes 133 amino acid residues. The deduced amino acid sequence showed duplicated Bowman-Birk type structure and active sites specific to trypsin, and it has relatively high homol. with those of proteinase inhibitors from wheat and bean. The new gene (RBBI) shares 74.8% homol. with a rice bran trypsin inhibitor reported previously. The evolutionary characteristics of the proteinase inhibitor family was also discussed.

IT **188900-56-3**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; cloning and sequencing of rice Bowman-Birk

proteinase inhibitor gene RBBI)

L3 ANSWER 29 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1997:97718 CAPLUS
DOCUMENT NUMBER: 126:170411
TITLE: Vespid venom hyaluronidase, phospholipase, or other enzyme as allergen, cDNA sequence and recombinant production of hyaluronidase, and allergy diagnosis and treatment
INVENTOR(S): King, Te P.
PATENT ASSIGNEE(S): The Rockefeller University, USA
SOURCE: U.S., 55 pp. Cont.-in-part of U. S. Ser. No. 31,400 abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5593877	A	19970114	US 1994-180209	19940111
WO 9420623	A1	19940915	WO 1994-US2629	19940310
W: AU, BB, BG, BR, BY, CA, CN, CZ, FI, HU, JP, KP, KR, KZ, LK, LV, MG, MN, MW, NO, NZ, PL, RO, RU, SD, SK, UA, UZ, VN				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9464041	A1	19940926	AU 1994-64041	19940310
AU 693785	B2	19980709		
EP 688362	A1	19951227	EP 1994-911550	19940310
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 08508399	T2	19960910	JP 1994-520320	19940310
US 5612209	A	19970318	US 1995-385745	19950208
PRIORITY APPLN. INFO.:			US 1993-31400	19930311
			US 1994-180209	19940111
			WO 1994-US2629	19940310

AB The present invention is directed to nucleic acids encoding vespid venom enzymes, or fragments thereof, recombinant vectors comprising such nucleic acids, and host cells contg. the recombinant vectors. The invention is further directed to expression of such nucleic acids to produce recombinant vespid venom enzymes, or recombinant fragments, derivs. or analogs thereof. Such recombinant products are useful for diagnosis of allergy and for therapeutic treatment of allergy. In specific embodiments, the present invention provides nucleic acids encoding, and complete nucleotide and amino acids sequences for, vespid venom phospholipase, for example, Dolichovespula maculata phospholipase and Vespula vulgaris phospholipase, and vespid venom hyaluronidase, for example, Dolichovespula maculata hyaluronidase.

IT **186986-50-5**
RL: ANT (Analyte); BPR (Biological process); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)
(nucleotide sequence; vespid venom hyaluronidase, phospholipase, or other enzyme as allergen, cDNA sequence and recombinant prodn. of hyaluronidase, and allergy diagnosis and treatment)

L3 ANSWER 30 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1995:569921 CAPLUS
DOCUMENT NUMBER: 123:219957
TITLE: The DNA sequence of human herpesvirus-6: structure, coding content, and genome evolution
AUTHOR(S): Gompels, U. A.; Nicholas, J.; Lawrence, G.; Jones, M.; Thomson, B. J.; Martin, M. E. D.; Efstathiou, S.;
Searched by Barb O'Bryen, STIC 308-4291

Craxton, M.; Macaulay, H. A.
CORPORATE SOURCE: Dept. Clinical Sci., London Sch. Hygiene and Tropical Med., London, WC1E 7HT, UK
SOURCE: Virology (1995), 209(1), 29-51
CODEN: VIRLAX; ISSN: 0042-6822
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The complete DNA sequence was detd. for strain U1102 of human herpesvirus-6, a CD4+ T-lymphotropic virus with disease assocns. in immunodeficient settings and a possible complicating factor in AIDS. The genome is 159,321 bp in size, has a base compn. of 43% G + C, and contains 119 open reading frames. The overall structure is 143 kb bounded by 8 kb of direct repeats, DRL (left) and DRR (right), contg. 0.35 kb of terminal and junctional arrays of human telomere-like simple repeats. Since eight open reading frames are duplicated in the repeats, six span repetitive elements and three are spliced, the genome is considered to contain 102 sep. genes likely to encode protein. The genes are arranged colinearly with those in the genome of the previously sequenced betaherpesvirus, human cytomegalovirus, and has a distinct arrangement of conserved genes relative to the sequenced gammaherpesviruses, herpesvirus saimiri and Epstein-Barr virus, and the alphaherpesviruses, equine herpesvirus-1, varicella-zoster virus, and herpes simplex virus. Comparisons of predicted amino acid sequences allowed the functions of many human herpesvirus-6 encoded proteins to be assigned and showed the closest relation in overall no. and similarity to human cytomegalovirus products, with approx. 67% homologous proteins as compared to the 21% identified in all herpesviruses. The features of the conserved genes and their relative order suggested a general scheme for divergence among these herpesvirus lineages. In addn. to the "core" conserved genes, the genome contains four distinct gene families which may be involved in immune evasion and persistence in immune cells: two have similarity to the "chemokine" chemotactic/proinflammatory family of cytokines, one to their peptide G-protein-coupled receptors, and a fourth to the Ig superfamily.

IT **167975-92-0**
RL: PRP (Properties)
(amino acid sequence; DNA and encoded peptide sequences of human herpesvirus-6)

L3 ANSWER 31 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1993:206501 CAPLUS
DOCUMENT NUMBER: 118:206501
TITLE: Comparison of the structure and nucleotide sequences of vicilin genes of cocoa and cotton raise questions about vicilin evolution
AUTHOR(S): McHenry, Lauren; Fritz, Paul J.
CORPORATE SOURCE: Dep. Food Sci., Pennsylvania State Univ., University Park, PA, 16802, USA
SOURCE: Plant Mol. Biol. (1992), 18(6), 1173-6
CODEN: PMBIDB; ISSN: 0167-4412
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Cocoa (Theobroma cacao) seeds produce two abundant mRNA transcripts during mid to late development. Approx. one-third of the abundant mRNA encodes a protease inhibitor (asp, abundant seed protease inhibitor); the other two-thirds encode a seed storage protein, cocoa seed vicilin (csv). The nucleotide sequence of a partial cDNA, and that of the gene covering the protein coding region of the vicilin, differ by only one nucleotide substitution which does not alter the amino acid at that position. A comparison of the sequences reveals the presence of five short, AT-rich introns of between 90 and 112 nucleotides. The genomic sequence includes 609 and 512 nucleotides of 5' and 3' untranslated sequence, resp. A TATA box (TATAAAT) is centered 41 nucleotides upstream of the first nucleotide

of the cDNA. Also present in the 5' upstream region is the core sequence of a conserved promoter element known as the G box (CACGTG), which has been shown to be a site of nuclear protein binding activity in a wide variety of genes responding to a range of stimuli including ABA, wounding, and UV and visible light. The gene from cotton (which is a dicot and is classified in the same taxonomic order as cocoa Malvales) contains only four introns, while the cocoa gene has five.. All legume (dicot) vicilin genes examd. to date also have five introns, while those from monocots, wheat and maize, have four introns. On the other hand, another significant index of gene relatedness, ests. of the no. of nucleotide substitutions per site for the first three exons of five vicilin genes (cocoa, cotton, french bean, pea and soybean), are consistent with their phylogenetic placement, i.e. the cocoa and cotton vicilin sequences are more closely related to each other than they are to the vicilins of bean, pea or soy. It seems likely that a fifth intron was present in the protoangiosperm gene before the monocot/dicot split and that this intron was lost independently in cotton and monocots, perhaps due to (as yet, undeciphered) inherent instability of this region of the gene.

IT **147388-32-7 147388-33-8**
RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)

L3 ANSWER 32 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1993:186041 CAPLUS
DOCUMENT NUMBER: 118:186041
TITLE: Cloning and sequencing of a cDNA encoding the major storage proteins of Theobroma cacao. Identification of the proteins as members of the vicilin class of storage proteins
AUTHOR(S): Spencer, Margaret E.; Hodge, Rachel
CORPORATE SOURCE: Plant Sci. Ltd., Sheffield, S10 2TN, UK
SOURCE: Planta (1992), 186(4), 567-76
CODEN: PLANAB; ISSN: 0032-0935
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The major storage proteins, polypeptides of 31 and 47 kDa, from the seeds of cocoa (Theobroma cacao L.), have been identified and partially purified by preparative gel electrophoresis. The polypeptides were both N-terminally blocked, but some N-terminal amino-acid sequence was obtained from a cyanogen bromide peptide common to both polypeptides, permitting the construction of an oligonucleotide probe. This probe was used to isolate the corresponding cDNA clone from a library made from poly(A)+ RNA from immature cocoa beans. The cDNA sequence has a single major open reading frame that translates to give a 566-amino acid polypeptide of Mr 65,612. The existence of a common precursor to the 31- and 47-kDa polypeptides of this size was confirmed by immunopptn. from total poly(A)+ RNA translation products. The precursor has an N-terminal hydrophobic sequence which appears to be a typical signal sequence, with a predicted site of cleavage 20 amino acids after the start. This is followed by a very hydrophilic domain of .apprx.110 amino acids, which, by analogy with the cottonseed .alpha.-globin, is presumed to be cleaved to leave a domain of approx. 47 kDa, very close to the obsd. size of the mature polypeptide. Like the hydrophilic domain of the cottonseed .alpha.-globin, the cocoa hydrophilic domain is very rich in glutamine and charged residues (esp. glutamate), and contains several Cys-X-X-X-Cys motifs. The cyanogen bromide peptide common to the 47-kDa and 31-kDa polypeptides is very close to the proposed start of the mature domain, indicating that the 31-kDa polypeptide arises via further C-terminal processing. The polypeptide sequence is homologous to sequences of the vicilin class of storage proteins, previously found only in legumes and cotton. Most of these proteins have a mature polypeptide size of approx. 47 kDa, and are

synthesized as precursors only slightly larger than this. Some, however, are larger polypeptides (e.g. .alpha.-conglycinin from soybean is 72 kDa), usually due to an addnl. N-terminal domain. In cottonseed, the situation appears to parallel that in cocoa in that the vicilin is synthesized as an approx. 70-kDa precursor and then processed to a 47-kDa (and in the case of cocoa also to a 31-kDa) mature protein. In this context, it is interesting that cotton is closer in evolutionary terms to cocoa than are the legumes, both cotton and cocoa being in the order Malvales.

IT **141961-55-9 147095-05-4**
RL: PRP (Properties)
(amino acid sequence of, complete)

L3 ANSWER 33 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1993:1730 CAPLUS
DOCUMENT NUMBER: 118:1730
TITLE: A cluster of four genes selectively expressed in the male germ line of Drosophila melanogaster
AUTHOR(S): Kuhn, Rainer; Kuhn, Claudia; Boersch, Dagmar; Glaetzer, Karl Heinz; Schaefer, Ulrich; Schaefer, Mireille
CORPORATE SOURCE: Inst. Genet., Heinrich-Heine-Univ., Duesseldorf, 4000/1, Germany
SOURCE: Mech. Dev. (1991), 35(2), 143-51
CODEN: MEDVE6; ISSN: 0925-4773
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The gene Mst87F is exclusively expressed in the male germ line and is subject to translational regulation. The Mst87F mRNA is transcribed in the primary spermatocytes, stored for 3 days and then subsequently translated in the post-elongation period of spermiogenesis. Here the isolation of a cluster of 4 small genes closely related in structure and function to Mst87F is reported. These genes are located at polytene band 84D on the right arm of chromosome and are named Mst84Da, Mst84Db, Mst84Dc and Mst84Dd. All 4 genes encode putative proteins composed primarily of a repetitive motif of cysteine-glycine-proline. The genes are exclusively expressed in the male germ line. The poly(A) tail of the Mst84D mRNAs increases in length at day 3 of pupal development, the time at which a similar change in Mst87F mRNA and translation has been shown to begin. In addn. a conserved 12 base pair element was identified within the 5' untranslated region (UTR) of each gene which is also found at an identical position in Mst87F and which has been demonstrated to be the structural element for translational control of Mst87F expression (Schaefer, U., et al., 1990). The gene cluster was mapped to a small deletion assocd. with a rotund mutation at 84D. Although flies with a homozygous deletion of the cluster still produce motile sperm, electron microscopic examn. revealed numerous malformations in the ultrastructure of the axoneme resulting in a drastic redn. of motile sperm.

IT **144905-07-7**, Protein (Drosophila melanogaster gene Mst84Db reduced) **144905-11-3**, Protein (Drosophila melanogaster gene Mst84Dd reduced)
RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)

L3 ANSWER 34 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1992:421504 CAPLUS
DOCUMENT NUMBER: 117:21504
TITLE: Cloning and expression of a cDNAs for a precursor of 47- and 31-kilodalton cocoa proteins
INVENTOR(S): Spencer, Margaret Elizabeth; Hodge, Rachel; Deakin, Edward Alfred; Ashton, Sean
PATENT ASSIGNEE(S): Mars G. B. Ltd., UK
Searched by Barb O'Bryen, STIC 308-4291

SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9119801	A1	19911226	WO 1991-GB914	19910607
W: AU, BR, CA, FI, GB, HU, JP, KR, NO, PL, RO, SU, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE				
CA 2084059	AA	19911212	CA 1991-2084059	19910607
AU 9179782	A1	19920107	AU 1991-79782	19910607
AU 659411	B2	19950518		
EP 535053	A1	19930407	EP 1991-911070	19910607
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
GB 2260328	A1	19930414	GB 1992-25934	19910607
BR 9106555	A	19930622	BR 1991-6555	19910607
JP 05507846	T2	19931111	JP 1991-510105	19910607
HU 65449	A2	19940628	HU 1992-3913	19910607
HU 216642	B	19990728		
PL 168506	B1	19960229	PL 1991-297176	19910607
PL 169122	B1	19960628	PL 1991-309174	19910607
PL 169958	B1	19960930	PL 1991-309173	19910607
NO 9204738	A	19930211	NO 1992-4738	19921208
US 5770433	A	19980623	US 1993-955905	19930121
PRIORITY APPLN. INFO.:			GB 1990-13016	19900611
			WO 1991-GB914	19910607

AB A cDNA encoding a 67-kDa protein that is the precursor of the 47- and 31-kDa major seed proteins of cocoa (Theobroma cacao), is cloned and expressed. The 47- and 31-kDa proteins were purified and used for prep. antibodies to identify the 67-kDa precursor. The 9 N-terminal amino acids of their CNBr-cleaved derivs., the 24- and 17-kDa peptides, were used for synthesizing oligonucleotide probes. The cDNA for the 67-kDa protein was obtained by screening the cDNA library of immature cocoa beans prepd. in the 3'-oligo(dG)-tailed pUC9. Seven expression plasmids for the 67kDa protein were prepd. and the expression of the cDNA in Escherichia coli or Saccharomyces cerevisiae was demonstrated.

IT **141961-55-9**
RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete, and cloning and expression in Escherichia coli or Saccharomyces cerevisiae of cDNA for)

L3 ANSWER 35 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1991:423434 CAPLUS
DOCUMENT NUMBER: 115:23434
TITLE: Serine-rich ultra high sulfur protein gene expression in murine hair and skin during the hair cycle [Erratum to document cited in CA114(11):96042m]
AUTHOR(S): Wood, Linda; Mills, Margo; Hatzenbuhler, Nicole; Vogeli, Gabriel
CORPORATE SOURCE: Upjohn Co., Kalamazoo, MI, 49001, USA
SOURCE: J. Biol. Chem. (1991), 266(6), 4024
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Errors in the DNA sequence in Figure 3 have been cor. The errors were reflected in the index entries.

IT **132212-43-2**, Protein UHS-SER 2 (mouse clone M16-8H reduced)
RL: PRP (Properties)

(amino acid sequence of (Erratum))

L3 ANSWER 36 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1991:137042 CAPLUS
DOCUMENT NUMBER: 114:137042
TITLE: Metallothionein Mto gene of Drosophila melanogaster: structure and regulation
AUTHOR(S): Silar, Philippe; Theodore, Laurent; Mokdad, Raja; Erraiss, Nour Eddine; Cadic, Agnes; Wegnez, Maurice
CORPORATE SOURCE: Lab. Embryol. Mol., Univ. Paris XI, Orsay, 91405, Fr.
SOURCE: J. Mol. Biol. (1990), 215(2), 217-24
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The sequence of the Mto gene, one of the 2 known metallothionein geens of D. melanogaster, is reported and compared with that of the other metallothionein gene, Mtn. The main structural features are the presence of a small intron (61 bp), the presence of 4 potential MREs (metal regulatory elements) and the absence of a TATA box in the promoter region. Of all metals tested, Hg2+, Cd2+ and Cu2+ are the most efficient ions for inducing an increase in Mto gene transcription. The Mto and Mtn genes are differentially regulated during normal development. Transcription of Mto is detected early in embryogenesis (0 to 3 h) and persists to the third larval instar, while Mtn expression starts later in embryogenesis (12 to 15 h) and is thereafter maintained throughout larval development and adult stages. Sequencing of the Mto protein is in good agreement with the nucleic acid data. Surprisingly, attempts to isolate and characterize the Mtn protein were unsuccessful. Several lines of evidence suggest that this metallothionein is rapidly incorporated after its synthesis into lysosomes, where it would be processed in a way that would not permit its purifn. The function of the Mtn protein thus appears to be mainly related to detoxification processes. The pattern of expression of Mto suggests that this gene may be involved in the control of metal homeostasis during development.
IT **109189-62-0**, Metallothionein (Drosophila melanogaster clone pCd2/pCd14 protein moiety reduced)
RL: PRP (Properties)
(amino acid sequence of)

L3 ANSWER 37 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1991:96042 CAPLUS
DOCUMENT NUMBER: 114:96042
TITLE: Serine-rich ultra high sulfur protein gene expression in murine hair and skin during the hair cycle
AUTHOR(S): Wood, Linda; Mills, Margo; Hatzenbuhler, Nicole; Vogeli, Gabriel
CORPORATE SOURCE: Upjohn Co., Kalamazoo, MI, 49001, USA
SOURCE: J. Biol. Chem. (1990), 265(34), 21375-84
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English
AB To study the regulation of hair differentiation, a murine genomic clone, gUHS-SER-M16, was isolated that contained 2 members of the family of serine-rich ultra-sulfur protein genes. One of the genes, gUHS-SER-1, encodes 230 amino acids with 40% cysteine and 23% serine; the other gene, gUHS-SER-2, encodes 223 amino acids with 41% cysteine and 21% serine. The similarity between the 2 genes is 73%, and both have several 10-amino acid repeats within their coding regions. In the prospective promoter region, there are several regions of similarity including a TATA box, with neither gene having a CAT box. At the 3' untranslated region, there is no similarity, and thus a fragment from this region was used as a hybridization probe for RNA dot-blots and for in situ hybridizations. The

RNA dot-blot showed elevated levels of mRNA during the active phases of hair growth and low levels during the resting phases. In situ hybridizations show that mRNA for the ultra-high-sulfur protein gene is found during the active phases of the hair cycle not only in the medulla and the inner root sheath of the forming hair but also in upper layers of the epidermis of skin.

IT **132212-43-2**, Protein UHS-SER 2 (mouse clone M16-8H reduced)
RL: PRP (Properties)
(amino acid sequence of)

L3 ANSWER 38 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1990:192271 CAPLUS
DOCUMENT NUMBER: 112:192271
TITLE: Substrate phosphorylation catalyzed by the insulin receptor tyrosine kinase. Kinetic correlation to autophosphorylation of specific sites in the .beta. subunit
AUTHOR(S): Flores-Riveros, Jaime R.; Sibley, Eric; Kastelic, Tania; Lane, M. Daniel
CORPORATE SOURCE: Sch. Med., Johns Hopkins Univ., Baltimore, MD, 21205, USA
SOURCE: J. Biol. Chem. (1989), 264(36), 21557-72
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The kinetics of insulin-stimulated autophosphorylation of specific tyrosines in the .beta. subunit of the mouse insulin receptor and activation of receptor kinase-catalyzed phosphorylation of a model substrate were compared. The deduced amino acid sequence of the mouse proreceptor was detd. to locate tyrosine-contg. tryptic peptides. Receptor was 1st incubated with unlabeled ATP to occupy nonrelevant autophosphorylation sites, after which [32P]autophosphorylation at relevant sites and attendant activation of substrate phosphorylation were initiated with [.gamma.-32P]ATP and insulin. Activation of substrate phosphorylation underwent an initial lag of 10-20s during which there was substantial [32P]autophosphorylation of tryptic phosphopeptides p2 and p3, but not p1. Following the lag, incorporation of 32P into p1 and activation of substrate phosphorylation increased abruptly and exhibited identical kinetics. The addn. of substrate to receptor prior ot ATP inhibits insulin-stimulated autophosphorylation, and consequently substrate phosphorylation. Insulin-stimulated autophosphorylation of the receptor in the presence of substrate inhibited primarily the incorporation of 32P into p1 and drastically inhibited substrate phosphorylation. From Edman radiosequencing of 32P-labeled p1, p2, and p3 and the amino acid sequence of the mouse receptor, the location of each phosphopeptide within the .beta. subunit was detd. Further characterization of these phosphopeptides revealed that p1 and p2 represent the triply and doubly phosphorylated forms, resp., of the region within the tyrosine kinase domain contg. tyrosines 1148, 1152, and 1153. The doubly phosphorylated forms contain phosphotyrosines either at positions 1148 and 1152/1153 or positions 1152 and 1153. Thus, insulin stimulates sequential autophosphorylation of tyrosines 1148, 1152, and 1153, and the transition from the doubly to the triply phosphorylated forms is primarily responsible for the activation of substrate phosphorylation.

IT **126649-13-6**
RL: PRP (Properties)
(amino acid sequence of)

L3 ANSWER 39 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1988:144435 CAPLUS
DOCUMENT NUMBER: 108:144435
Searched by Barb O'Bryen, STIC 308-4291

TITLE: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Sequences and genomic organization of the .alpha. globulin (vicilin) genes of cottonseed
AUTHOR(S): Chlan, Caryl A.; Borroto, Katyna; Kamalay, J. A.; Dure, Leon, III
CORPORATE SOURCE: Dep. Biochem., Univ. Georgia, Athens, GA, 30602, USA
SOURCE: Plant Mol. Biol. (1987), 9(6), 533-46
CODEN: PMBIDB; ISSN: 0167-4412
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The .alpha. globulin storage protein genes of cotton are found to exist as gene tandems that contain a gene from each of the 2 .alpha. globulin subfamilies sepd. by a spacer region of .apprxeq.2700 or 3400 base pairs. Three different tandems have been identified by restriction endonculease mapping of genomic DNA. A cDNA that is different from the genes of the tandems in map sites and(or) in nucleotide sequence indicates that a fourth tandem probably exists in the cotton genome. Since the species of cotton used here (Gossypium hirsutum) is an amphidiploid, it is likely that two of the tandems are contributed from each genome. Considerable divergence in nucleotide sequence (18%) and in derived amino acid sequence (28%) is found when the 2 genes of a sequenced tandem are compared. The sequence of the cDNA closely resembles one of the genes in the tandem showing only a 4% divergence in nucleotides and a 4.2% divergence in amino acids. Thus, the 2 genes of each tandem represent a relatively ancient gene duplication that has given rise to the 2 .alpha. globulin subfamilies of cotton. Only one subfamily has a glycosylation site and the glycosylation of its derived proteins gives rise to the 2 mol.-wt. sets of .alpha. globulins seen on gel electrophoresis. Other basic features of these genes and their derived proteins are presented.

IT **113670-42-1 113670-43-2 113670-44-3**
113670-45-4
RL: PRP (Properties)
(amino acid sequence of)

L3 ANSWER 40 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1987:528213 CAPLUS
DOCUMENT NUMBER: 107:128213
TITLE: Metallothionein genes in Drosophila melanogaster constitute a dual system
AUTHOR(S): Mokdad, Raja; Debec, Alain; Wegnez, Maurice
CORPORATE SOURCE: Cent. Genet. Mol., Cent. Natl. Rech. Sci., Gif-sur-Yvette, 91190, Fr.
SOURCE: Proc. Natl. Acad. Sci. U. S. A. (1987), 84(9), 2658-62
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A metallothionein (MT) cDNA clone was selected from a cadmium-resistant D. melanogaster cell line and sequenced. This clone includes an open reading frame coding for a 43-amino acid protein whose characteristics are a high cysteine content (12 cysteines, 28% of all residues) and a lack of arom. amino acids. This protein differs markedly from the Drosophila MT (Mtn gene) previously reported (Lastowski-Perry, D., et. al., 1985). Thus, the MT system of Drosophila consists of at least two distantly related genes, in sharp contrast with vertebrate MT systems, in which the different members of MT gene families display high similarity. The gene corresponding to this MT cDNA (Mto) is inducible in Drosophila cell lines and in both larval and adult flies.

IT **109189-62-0**
RL: PRP (Properties)
(amino acid sequence of)

L3 ANSWER 41 OF 41 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1987:44864 CAPLUS
DOCUMENT NUMBER: 106:44864
TITLE: Developmental biochemistry of cottonseed embryogenesis and germination. XVIII. cDNA and amino acid sequences of members of the storage protein families
AUTHOR(S): Chlan, Caryl A.; Pyle, J. B.; Legocki, A. B.; Dure, Leon, III
CORPORATE SOURCE: Dep. Biochem., Univ. Georgia, Athens, GA, 30602, USA
SOURCE: Plant Mol. Biol. (1986), 7(6), 475-89
CODEN: PMBIDB; ISSN: 0167-4412
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Some cDNA clones representing each of the 3 distinct groups of storage proteins of the cotton seed were sequenced. Characteristics of their mRNAs and derived proteins are given. Dot matrix anal. of the nucleotide and amino acid sequences shows that 2 of these groups of proteins have a great deal of vestigial homol. at low stringency and should be considered subfamilies of a single storage protein gene family. The remaining group is quite distinct and should be considered a sep. multigene family. It also can be divided into 2 subfamilies based on the presence or absence of glycosyl residues and other sequence differences. These proteins are processed to smaller species during embryogenesis, and all of the mature storage proteins of cotton can be traced back to these 2 gene families. In view of these relationships it is proposed that these 2 families be called the .alpha. and .beta. globulins of cotton storage proteins, each contg. an A and B subfamily.
IT **106387-99-9 106388-00-5**
RL: PRP (Properties)
(amino acid sequence of)

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